

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 00:49:36 ; Search time 4784.11 seconds
(without alignments)
1569.471 Million cell updates/sec

Title: US-09-698-781-3
Sequence: 1 MKQILHPALETTMTLPVL.....KHQVRSCKRSCNSNSIY 258

Scoring table: BIOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame+P2n.model -DEV-xml
-O/cgn2.1/USPTO-spool/US09698781/unat_07032003.083459.5322/app.query.fasta.1.654
-DB-genEmbl -OPMT-fastlap -SUFFIX-p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human4.0cd1 -LIST=45
-DOCALLIGN=200 -THR.SCORE-pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTPMT-pio -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09698781.qcgn.1.1.2566 -urnat_07032003.083459.5322 -NCPu=6 -ICPU=3
-NO_XLPHY -NO_MMAR -LANGUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV-TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_hcg:*
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16: em_fun:*
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20: em_om:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1436	100.0	2138	9	HSSPG28	X94322 H.sapiens m
2	1436	100.0	2144	6	AX127587	AX127587 Sequence
3	1386	96.5	2128	6	AX335634	AX335634 Sequence
4	1386	96.5	2128	9	HSCRISP3G	X95240 H.sapiens m
5	1002	69.8	1335	9	HUMTPX1A	M25532 Human testis
6	1002	69.8	1380	9	BC022011	BC022011 Homo sapi
7	1002	69.8	1406	9	HSCRISP21	X95239 H.sapiens m
8	982.5	68.4	1388	10	CPU35712	U35712 Cavia porcea
9	952.5	66.3	1295	4	ECCRISP3	AJ001400 Equus caballus
10	856	59.6	1280	10	AB009662	AB009662 Rattus norvegicus
11	853	59.4	1432	10	AF078552	AF078552 Rattus norvegicus
12	835	58.1	1418	10	MUSTPX1A	M25533 Mouse testis
13	772.5	53.8	1380	10	MUSARGLA	M92849 Mouse testis
14	772.5	53.8	1403	10	MUSARGLA	L05539 Mouse cysteine
15	760.5	53.0	1445	10	BC011150	BC011150 Mus musculus
16	759.5	52.9	928	10	RNESGR	X04643 Rat mRNA for
17	759.5	52.9	1498	10	RATARG	M31173 Rat epididymis
18	684	47.6	495	4	ECAR632	AJ006632 Equus caballus
19	677.5	47.2	1090	5	U13619	U13618 Heloderma
20	669	46.6	1336	5	AF384218	AF384218 Agkistrodon
21	656	45.7	791	5	AY093955	AY093955 Rhabdophis
22	650.5	45.3	1331	5	AF384219	AF384219 Trimeresurus
23	650	45.3	1318	5	PMU59447	PMU59447 Trimeresurus
24	637.5	44.4	1305	5	AF384220	AF384220 Laticauda
25	627.5	43.7	1309	5	AF190861	AF190861 Lapemis
26	625.5	43.6	1394	10	MUSARGLA	M28850 Mouse cysteine
27	625.5	43.6	1406	10	MUSARGLA	L05560 Mouse cysteine
28	625.5	43.6	1418	10	BC023573	BC023573 Mus musculus
29	612.5	42.7	1316	5	AF159541	AF159541 Lapemis
30	590.5	41.1	433	4	BT277708	BT277708 Bos taurus
31	542.5	37.8	1343	9	AF123894	AF123894 Macaca
32	542	37.7	1475	4	EC315379	EC315379 Equus
33	529.5	36.9	1281	9	HUMARP	D38451 Homo sapiens
34	529.5	36.9	1282	9	S80310	S80310 acidophilic
35	529.5	36.9	1886	9	HSCRISP1G	X95237 H.sapiens m
36	525	36.6	1174	4	ECAR631	AJ006631 Equus caballus
37	463	32.2	334	4	BT277709	BT277709 Bos taurus
38	406.5	28.3	1797	9	HSCRISP1D	X95238 H.sapiens m
39	366	25.5	151752	2	AC010779	AC010779 Homo sapiens
40	358	24.9	758	5	AF393653	AF393653 Xenopus
41	358	24.9	90901	9	HS1417120	AL121974 Human DNA
42	350.5	24.4	1025	10	BC025083	BC025083 Mus musculus
43	345	23.5	1008	6	AX376552	AJ006635 Sus scrofa
44	337.5	23.5	1008	6	AX376552	AX376552 Sequence
45	329	22.9	873	9	AF400440	AF400440 Homo sapiens

RESULT 1

ALIGNMENTS

[illegible]

OY	101	LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer	120
Db	302	AAGGATTCGAATGACAAAGTCTAAAGTGTGGGAATCTCTACATGTCAAGTGGCCCCAGC	361
OY	121	SerTPSerGlnAlaIleGlnSerTPPheAspGluTyrAsnAspPheAspPheGlyVal	140
Db	362	TCATGTCACAAAGCAATCCAAAGCGGTTTGTATGATGCATCAATGATTTTGACCTGGTGA	421
OY	141	GlyProLysThrProAsnAlaValAlaGlyHisTyrThrGlnValValITPtyrSerSer	160
Db	422	GGGCCAAAGACATCCCAAGCAGTGGTTGGACATTTATACAGAGGTGGTGGTACCTTCA	481
OY	161	TyrLeuValAlaGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyr	180
Db	482	TACCTCGTTGGATGTGGGAATGCCACTGCTCCATCATCAAAAAGTCTAAATATCACTAT	541
OY	181	ValCysGlnTyrCysProAlaGlyAsnTPAlaAsnArgLeuTyrValIProTyrGln	200
Db	542	GTTTCCCAATATGTCCTCGCTGGTAATGGCTTAATACATATATGCTCTATCAACA	601
OY	201	GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys	220
Db	602	GGAGACCTTGTGGCAGATGGCCCAATATACATGTGCATGTGCATATGCACCAATGGTTC	661
OY	221	LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis	240
Db	662	AAGTACGAAGATCTCTATAGTACTGTAAAGATTGAAGCTCACATTAACCTGTAAACAT	721
OY	241	GlnLeuValAlaArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr	258
Db	722	CAGTTGGTCAGGAGCAGTGCAGAGGCCCTCTGCATTTGTTCAAACAGCATTTAT	775
RESULT 2			
LOCUS	AX127587	2144 bp	DNA
DEFINITION	Sequence 2 from Patent WO0131343.		Linear
ACCESSION	AX127587		
VERSION	AX127587.1		GI:14134279
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2144) Huber,R.S., Raitano,A.B., Afar,D.E., Mitchell,S.C., Farris,M. and Jakobovits,A.		
TITLE	Diagnosis and therapy of cancer using sgp28-related molecules		
JOURNAL	Patent: WO 0131343-A 2 03-MAY-2001.		
FEATURES	Urogenesys, Inc. (US)		
Source	Location/Qualifiers		
BASE COUNT	1. 2144 /organism="Homo sapiens" /db_xref="taxon:9606"		
ORIGIN	735 a 403 c 382 g 624 t		
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Score:	1436.00	Matches:	258
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-698-781-3 (1-258) x AX127587 (1-2144)			
OY	1	MettysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu	20
Db	3	ATGAACAACAAATACCTTCATCTCTGCTGGAAACACATGCAATGACATTTATCCACTGCTG	62
OY	21	LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla	40
Db	63	TGTGTCCTGCGTGTGCGGCTGCTTCATCTTTTCACGAACATGAAGATTAAGATCCGCT	122

QY 41 PheThAlaLeuLeuThrThrGlnThrGlnValGlnArgGluLeuValaLeuLysHisAsn 60
 DB 123 TTTACTGCTTTGTTAAACCCCAACACAGTCCAAAGGAGATTGTGAATTAAGCACAAAT 182
 QY 61 GtLeuValArgAlaValSerProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
 DB 183 GAACTAGAGGAGACAGTATCTCCCTGCCAGAAACATGCTGAAGATGGAATGGAACAAA 242
 QY 81 GtAlaAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTrpArgHisSerAsnPro 100
 DB 243 GAGGCTGCAGCAAAATGCCCAAAAGTGCGCAACAGTGCATTAACAGACAGTAAACCCA 302
 QY 101 LysAspArgMetThrSerLeuLysCysGlyGlnAsnLeuLysMetSerAlaProSer 120
 DB 303 AAGGATCGAATGACAAAGTCTAAATGCTGAGAAATCTCAATGTCAGTCCGCCAGC 362
 QY 121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTrpAsnAspPheAspPheGlyVal 140
 DB 363 TCATGCTCACAAACCAATCCAAAGCTGTTGATGAGTACATGATTTTGACTTTGGTGA 422
 QY 141 GlyProLysThrProAsnAlaValAlaGlyHisTrpThrGlnValValIleTrpTyrSerSer 160
 DB 423 GGGCCAAAGACTCCCAACCGAGTGTGACATTAACACAGTGTGTTGGTACTCTTCA 482
 QY 161 TyrLeuValGlyCysGlyAsnAlaIleTrpCysProAsnGlnLysValLeuLysTrpTyr 180
 DB 483 TACCTGCTGATGATGGAATGCTTACTGTCACATCAAAAAGTCTTAAATACTACTAT 542
 QY 181 ValCysGlnTrpCysProAlaGlyAsnTrpAlaAsnArgLeuTrpValProTyrGluGln 200
 DB 543 GTTGGCAATATATGCTCTGCTGTAATGGCTAATAGACTATATATGCCCTTAAGAACAA 602
 QY 201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysTrpAsnGlyCys 220
 DB 603 GGAGACACTTGTCTCCACTTCCAGATACACTGTGCACATGACATATACCACAAATGGTTGC 662
 QY 221 LysTrpGlnAspLeuLysTrpSerAsnCysLysSerLeuLysLeuThrCysLysHis 240
 DB 663 AAGTACAGAAATCTCTATAGTAACTGTAAAGTTGAAGCTCACATTAACCTGTAAACAT 722
 QY 241 GtLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
 DB 723 CAGTGTCTCAGGAGCACTTCCAAAGCATCTCTGCAATTTGTTCAACACATTTAT 776
 RESULT 3
 AX335634 2128 bp DNA linear PAT 09-JAN-2002
 LOCUS AX335634
 DEFINITION Sequence 6143 from Patent WO0194629.
 ACCESSION AX335634
 VERSION AX335634.1 GI:18126353
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
 Horigan, S., Soppet, D. R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
 gene sets
 Patent: WO 0194629-A 6143 13-DEC-2001;
 JOURNAL Avalon Pharmaceuticals (US)
 FEATURES
 source Location/Qualifiers
 1..2128
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 734 a 397 c 380 g 617 t
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 Alignment Scores: 3.68e-131 Length: 2128
 Pred. No.: 1386.00 Matches: 249
 Score:

Percent Similarity: 99.608
 Best Local Similarity: 99.608
 Query Match: 96.528
 DB: 6 Gaps: 0
 US-09-698-781-3 (1-258) x AX335634 (1-2128)
 QY 9 LeuGluThrThralaMetThrLeuPheProValLeuLeuPheLeuValaGlyLeuLeu 28
 DB 1 CTGGAAACCACTCATGATGATATTCGCCAGTCTGTGTCTGCTGGTGGCTGCTT 60
 QY 29 ProSerPheProAlaAsnGluAspLysAspProAlaPheThralaLeuLeuThrGln 48
 DB 61 CCATCTTTCCACCAATGAAGATGAAGATGCCGCTTTTACTCTTGTGTTAAACCCCAA 120
 QY 49 ThrGlnValGlnArgGluLeuValaAsnLysHisAsnGluLeuArgArgAlaValSerPro 68
 DB 121 ACACAGTGCMAAGGAGGATGTGAATMACACAAATGAACTGAGAGAGACGATCTCC 180
 QY 69 ProAlaArgAsnMetLeuLysMetGluTrpAsnLysGlnAlaAlaAsnAlaGlnLys 88
 DB 181 CTGTCACGAACATCTCTGAAGATGGAATGCAACAAAGAGCTGCAGCAAAATGCCAAAAG 240
 QY 89 TrpAlaAsnGlnCysAsnTrpArgHisSerAsnProLysAspArgMetThrSerLeuLys 108
 DB 241 TGGGCAAAACAGTGCATTAACAGACAGTAAACCAAGATGGAATGACAAAGCTTAA 300
 QY 109 CysGlyGlnAsnLeuLysMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSer 128
 DB 301 TGTGGTGAATCTCTAACAAGTCAAGTCCCAAGCTCATGATGTCACAAAGATCCAAAGC 360
 QY 129 TrpPheAspGluTrpAsnAspPheAspPheGlyValGlyProLysThrProAsnAlaVal 148
 DB 361 TGGTTTATAGTACAAATGATTTTGACTTTGGTGTAGGCCAAAGACTCCCAACGAGTG 420
 QY 149 ValGlyHisTrpThrGlnValValIleTrpTyrSerSerTrpLeuValGlyCysGlyAsnAla 168
 DB 421 GTTGGACATTAACACAGAGTGTGTTGTACTCTTCATACCTCGTTGATGTGAAATGCC 480
 QY 169 TyrCysProAsnGlnLysValLeuLysTyrTrpTyrValCysGlnTrpCysProAlaGly 188
 DB 481 TACGTCTCCATCAAAAAGTCTTAAATACTACTATTTTGGCAATTTTCTCTGCTGCT 540
 QY 189 AsnTrpAlaAsnArgLeuTrpValProTyrGluGlnGlyAlaProCysAlaSerCysPro 208
 DB 541 AATTGGCTATATAGCTATATGTCCTTATGACAAAGACACACTTGTCCAGTGGCCA 600
 QY 209 AspAsnCysAspAspGlyLeuCysTrpAsnGlyCysLysTrpGluAspLeuTyrSerAsn 228
 DB 601 GATNACTGTGACATGAGTACATATGACCAATGTTGCAAGTGCAGAAATCTCTATAGTAAC 660
 QY 229 CysLysSerLeuLysLeuThrLeuThrCysLysHisGlnLeuValaArgAspSerCysLys 248
 DB 661 TGTAAAGTTGAAGCTCACTTAACCTGTAAACATGAGTGTGCAGGAGACAGTTGCAAG 720
 QY 249 AlaSerCysAsnCysSerAsnSerIleTyr 258
 DB 721 GCTCTCTGCAATTTGTTCAACACAGCATTTAT 750
 RESULT 4
 HSCRISP3G 2128 bp mRNA linear PRI 12-APR-1996
 LOCUS H. sapiens mRNA for cysteine-rich secretory protein-3.
 DEFINITION X95240
 ACCESSION X95240.1 GI:1262818
 VERSION X95240.1 GI:1262818
 KEYWORDS CRISP-3 gene; cysteine-rich secretory protein-3.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2128)
 Kratzschmar, J., Haendler, B., Eberspaecher, U., Roosterman, D.,
 Donner, P. and Schleuning, W.D.

TITLE The human cysteine-rich secretory protein (CRISP) family. Primary structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3

JOURNAL Eur. J. Biochem. 236 (3), 827-836 (1996)

MEDLINE 96270732

PUBMED 8665901

REFERENCE 2 (bases 1 to 2128)

AUTHORS Haendler, B.

TITLE Direct Submission

JOURNAL Submitted (18-JAN-1996) B. Haendler, Schering AG, ICMB, S109/517, 13342 Berlin, FRG

FEATURES

source location/Qualifiers

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/db_xref="taxon:9606"

/clone_lib="testis cDNA library"

16..753

/gene="CRISP-3"

16..753

/gene="CRISP-3"

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/gene="CRISP-3"

polya_signal 2084..2089

BASE COUNT 734 a 397 c 380 g 617 t

ORIGIN

Alignment Scores:

Pred. No.: 3.68e-131 Length: 2128

Score: 1386.00 Matches: 249

Percent Similarity: 99.60% Conservative: 0

Best Local Similarity: 99.60% Mismatches: 1

Query Match: 96.52% Indels: 0

DB: 9 Gaps: 0

US-09-698-781-3 (1-258) x HSCRISP3C (1-2128)

Oy 9 LeuGIuTrThrAlaMetThrIleuPheProValIleuPheLeuValAlaGlyLeu 28

Db 1 CTGGAAACCACTGCATATCCATTTCCAGTGTGTTCTCGTGGCTGCTT 60

Oy 29 ProSerPheProAlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrGln 48

Db 61 CCATCTTTCGCAAGATGAAGATAGGATCCGCTTTTACGCTTTGTATACCAACCA 120

Oy 49 ThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArgAlaValSerPro 68

Db 121 ACACAGAGCAAGAGGAGATGTGATAGCAATGAAGTGAAGAGAGCACTATCTCC 180

Oy 69 ProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAlaAsnAlaGlnLys 88

Db 181 CCTGCCAACAACATCTCTGAAGATGGAATGAACAAAGAGGCTGCAGCAATGCCAAG 240

Oy 89 TrpAlaAsnGlnCysAsnTrpArgHisSerAsnProLysAspArgMetThrSerLeuLys 108

Db 241 TGGGCAACCAAGTGCATATACAGACAGTAAACCAAGATGCAATGACAGTCAAAAG 300

Oy 109 CysGlyGluAsnLeuTrpMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSer 128

Db 301 TGTGTGAGAACTCTTACATGCAAGTGCCTCAGCTCATGTGTCAACAGCAATCCAAAGC 360

Oy 129 TrpPheAspGluTrpAsnAspPheAspPheGlyValGlyProLysThrProAsnAlaVal 148

Db 361 TGGTTGATGAGTACAAATGATTTTACCTTGTGTGTAGGAGCCAAAGACTCCCAAGCAGTG 420

Oy 149 ValGlyHisTyrThrGlnValAlaTrpTyrSerSerTyrLeuValGlyCysGlyAsnAla 168

Db 421 GTTGACATATACACAGAGTGTGTGATCTCTTACCTGCTGGATGAGTGAATGCGC 480

Oy 169 TyrCysProAsnGlnLysValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGly 188

Db 481 TACTGTCCCAATCAAAAGATCTTAATAATCTACTATGTGTGCAATATGTCTCTCGT 540

Oy 189 AsnTrpAlaAsnArgLeuTrpValProTyrGluGlnGlyAlaProCysAlaSerCysPro 208

Db 541 AATTGGGCTAATAGACTATATATCTCTTGTGACAAAGAGCACTTGTCCAGTTGCCA 600

Oy 209 AspAsnCysAspAspGlyLeuLysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsn 228

Db 601 GATACTGACAGATGAGACTATGACCAATGGTGCAGTACGAAGATCTATAGTAAAC 660

Oy 229 CysLysSerLeuLysLeuThrIleuThrCysLysHisGlnLeuValArgAspSerCysLys 248

Db 661 TGTAAAGTTTGAAGCTCATTAACCTGTAAACATCACTGTGTCAGGACAGTTGCAAG 720

Oy 249 AlaSerCysAsnCysSerAsnSerIleTyr 258

Db 721 GCCTCTCGCAATTTGTTCAACAGCATTTAT 750

RESULT 5

HUMTPX1A

LOCUS HUMTPX1A 1335 bp mRNA linear PRI 14-JAN-1995

DEFINITION Human testis-specific protein (Tpx-1) mRNA, complete cds.

ACCESSION M25532 J04741

VERSION M25532.1 GI:339882

KEYWORDS testis-specific protein.

SOURCE Human adult testis, cDNA to mRNA, clones H4-1 and p3-1.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1335)

AUTHORS Kasahara, M., Gutknecht, J., Brew, K., Spurr, N. and Goodfellow, P. N.

TITLE Cloning and mapping of a testis-specific gene with sequence similarity to a sperm-coating glycoprotein gene

JOURNAL Genomics 5 (3), 527-534 (1989)

MEDLINE 90129048

PUBMED 2613236

COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by M. Kasahara, 09-JUN-1989.

FEATURES

source location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="6p21-qter"

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/gene="GAPDL5"

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/product="testis-specific protein mRNA"

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/note="testis-specific protein precursor"

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190..249

/gene="GAPDL5"

/note="testis-specific signal peptide (put.); putative"

250..918

/gene="GAPDL5"

/product="testis-specific protein (put.); putative"

sig_peptide

mat_peptide

BASE COUNT 428 a 279 c 271 g 355 t 2 others

ORIGIN Chromosome 6.

Alignment Scores: 2,46e-92 Length: 1335
 Pred. No.: 1002.00 Matches: 184
 Score: 80.84% Conservative: 27
 Percent Similarity: 80.84% Mismatches: 45
 Best Local Similarity: 70.50% Indels: 5
 Query Match: 69.78% Gaps: 3
 DB: 9

US-09-698-781-3 (1-258) x HUMPEX1A (1-1335)

Oy 1 MetysglnlleuHISProAlaLeuGlnThr-Thr-----AlaMetThrLeuPhePr 18
 Db 144 ATAAAGTAGATATTTCCTCCTCAGAAACCAACATTTCCAGCATGGCTTTACTAC 203
 Oy 18 ovalleuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
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 Db 258 TCCGCGCTTACTGCTGTTGTAACCCACCTGCACACTGCACAAAGGAGATTGTAAATTA 317
 Oy 58 SHIASnglLeuArgrArgrAlaValaSerProProAlaArgrAsnMetLeuLysMetGluTr 78
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 Oy 98 rAsnProLysAspArgMetThrSerLeuLysGlyLysLysLysLysLysLysLysLys 118
 Db 438 TGATTCACAGAGACCGCAAAACAGTACAGATGTGTGAGATCTCTATATGTCAAGTGA 497
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 Oy 218 nGlyCysLysTrpGluAspLeuTrpSerAsnCysLysSerLeuLysLeuThrLeuThCy 238
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 Oy 238 sLysHisGlnLeuValAlaGspSerCysLysAlaSerCysAsnCysSerAsnSerIleTy 258
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 Oy 258 r 258
 Db 918 C 918

RESULT 6

LOCUS BC022011 1380 bp mRNA linear PRI 24-JAN-2002
 DEFINITION Homo sapiens, testis specific protein 1 (probe H4-1 p3-1), clone
 MGC:26358 IMAGE:4826427, mRNA, complete cds.

ACCESSION BC022011
 VERSION BC022011.1 GI:18314472
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1380)
 Strausberg, R.
 Direct Submission
 Submitted (22-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansystemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whitting

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 Clone distribution: MGC clone distribution information can be found
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 Series: IRAC Plate: 33 Row: n Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4507670.

FEATURES

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CDS

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 Percent Similarity: 80.84% Mismatches: 45
 Best Local Similarity: 70.50% Indels: 5
 Query Match: 69.78% Gaps: 3
 DB: 9

US-09-698-781-3 (1-258) x BC022011 (1-1380)

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 Oy 18 ovalleuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
 Db 233 GGTG---TTGTTTCTGCTTACTGTGCTGCTTCATCTTACTCTGA---GAAGGAAAGGA 286

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Oy 78 pAsnLysGluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyraGHisSe 98
Db 407 GAGCAGAGAGAGTAAACAGAGATGCCAAAGTGGGCAAAAGTGCACCTTACACATRG 466
Oy 98 rAsnProLysAspArgMetThrSerLeuLysCysGlyLysAsnLeuTyrmSerSerAl 118
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Oy 238 sLysHisGlnLeuValArgAspSerCysLysSerCysAsnCysSerAsnSerLysTy 258
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LOCUS H.sapiens mRNA for cysteine-rich secretory protein-2/type I.
DEFINITION X95239
ACCESSION X95239.1 GI:1262816
VERSION CRISP-2 gene; cysteine-rich secretory protein-2/type I.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1406)
AUTHORS Kratzschmar,J., Haendler,B., Eberspacher,U., Roosterman,D.,
Donner,P. and Schleuning,W.D.
TITLE The human cysteine-rich secretory protein (CRISP) family. Primary
structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3
JOURNAL Eur. J. Biochem. 236 (3), 827-836 (1996)
MEDLINE 96270732
PUBMED 8665901
REFERENCE 2 (bases 1 to 1406)
AUTHORS Haendler,B.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1996) B. Haendler, Schering AG, ICBM, S109/517,
13342 Berlin, FRG
COMMENT Related sequence J04741.

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Score: 1002.00 Matches: 184
Percent Similarity: 80.84% Conservative: 27
Best Local Similarity: 70.50% Mismatches: 45
Query Match: 69.78% Indels: 5
DB: 9 Gaps: 3
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Oy 58 SH1sAngluLeuAArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTr 78
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[illegible]

TITLE Direct Submission
JOURNAL Submitted (03-SEP-1997) Schambony A., Institut fuer Reproduktionsmedizin, Tierärztliche Hochschule Hannover, Bunteleweg 15, D-30559 Hannover, GERMANY
REFERENCE 2 (bases 1 to 1295)
AUTHORS Magdaleno, L., Gasset, M., Varela, J., Schambony, A. M., Urbanke, C., Rada, M., Topfer-Petersen, E. and Calvete, J. J.
TITLE Biochemical and conformational characterisation of HSP-3, a stallion seminal plasma protein of the cysteine-rich secretory protein (CRISP) family
JOURNAL FEBS Lett. 420 (2-3), 179-185 (1997)
MEDLINE PUBMED 98119394
FEATURES 9459306

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Query Match: 66.33% Indels: 3
DB: 4 Gaps: 3

US-09-698-781-3 (1-258) x ECCRISP3 (1-1295)

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DEFINITION AB009662
ACCESSION AB009662
VERSION AB009662.1 GI:3374579
KEYWORDS testis specific protein.
SOURCE Rattus norvegicus (strain:Donryu) 20 days after birth male Testis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1280)
Maeda, T., Sakashita, M., Ohba, Y. and Nakanishi, Y.
Molecular cloning of the rat Tpx-1 responsible for the interaction between spermatogenic and Sertoli cells
Biochem. Biophys. Res. Commun. 248 (1), 140-146 (1998)
JOURNAL 9840864
MEDLINE 9840864
REFERENCE 2 (bases 1 to 1280)
AUTHORS Nakanishi, Y.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-1997) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences, 13-1 Takara-machi, Kanazawa, Ishikawa 920, Japan (Tel:076-234-4480, Fax:076-234-4480)
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ACCESSION			L05559
VERSION			L05559.1
KEYWORDS			GI:309190
SOURCE			
ORGANISM			Mus musculus
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			Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			1 (bases 1 to 1403)
AUTHORS			Haendler,B., Kratzschmar,J., Theuring,F. and Schluning,W.D.
TITLE			Transcripts for cysteine-rich secretory protein-1 (CRISP-1); DE/ABG
			and the novel related CRISP-3 are expressed under androgen control
			in the mouse salivary gland
JOURNAL			Endocrinology 133 (1), 192-198 (1993)
MEDLINE			93307144
PUBMED			8319566
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Fri Mar 14 14:00:08 2003

us-09-698-781-3.p2n.rge

Page 13

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Oy	70	ALAARGASNMETLEULYSMETGLUTPRASNLYSGULNALAALASANALAGINTSTP	89
Db	207	GGCAGTACTACTACTAAAAATGCAATGGAAGTACTATGATCTCTCAAGTGAATGCTCAGCAATG	266
Oy	90	ALAASNGINCYASANTYRARGHISSEASNPOLYASAPRGMECHRSETRLEULYS	109
Db	267	GCACACCAAGTGTACATTCTCAGTCACACAGTCCTATGAACTCGAGCACTAATTTAAATGTG	326
Oy	110	GLYGLVSNLEULYRMESETSERSEALAPROSESETRTPSERGINALALLEGINSERTP	129
Db	327	GGGGAGATTCTTTCATGTCATCTTCACTTGCAATCATGCTCTTCTGCAATCCAAAGCATGG	386
Oy	130	PHASPGIUTYRASNASPPHASPHEGLIYALGLYPROLYSTRPROASNALAVAL	149
Db	387	TATATGAATCAAAAGACTCTTACATGATGATGGTGGCCCAAGCAACTGATAGTGGTGC	446
Oy	150	GLYHSTRYTHRGINVALITPTPTYSERSETRYLEULVALGLCYSGSYASNALATYR	169
Db	447	GGACATTAATCTCAGGTGGTTTGGAACTCTTCACTTCCAACTGTCATGTGAGTTGGTGA	506
Oy	170	CYSPROASNGINLYSVALLEULYSYTRYTYTLYVALCYSGINTRYCYSPROALAGLYASN	189
Db	507	TGGCCT---AAAATCCACTGAGTACTATATGTGTTGTGACTATGTCTCTGTTGGCAAT	563
Oy	190	TRPALASNAARGLEUTYRVALPTOTRYGLINGLYALAPCYCASALASERCYSPROASP	209
Db	554	TATCAAGAGAGCGATACACACCTTCACTGACGTGACAGAAACCGTGCCAGTTGGCCGAT	623
Oy	210	ASNCYASAPASPGIYLEUCYETHASNGLYCYLSYSTYTRGLUASPLEULYRYSERASNCYS	229
Db	624	CACGTGAGAGATGGGCTATGCACCAATAGTTGTGGACATGAAGATAGTATACAAACTGT	683
Oy	230	LYSSETRLEULYSLEUTHLEUTHCYLSYSHISGLINLEULVALARGASPSERCYSLYALA	249
Db	684	AAATATCTGGAAGAGACATCTCTCCGTGACATGACATCAACTTTAAAAAAGTTGCCAAAGCT	743
Oy	250	SERCYASANCYSSERASNSERILETRYR	258
Db	744	ACATGCTCTGTGAAGGCCAAATTTAC	770

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